

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
ROBERTS-RAPP, LISA
RUSSELL, JOHN C.
STROUPE, STEPHEN D.

(ii) TITLE OF THE INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE PROSTATE

(iii) NUMBER OF SEQUENCES: 33

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Abbott Laboratories
(B) STREET: 100 Abbott Park Road
(C) CITY: Abbott Park
(D) STATE: IL
(E) COUNTRY: USA
(F) ZIP: 60064-3500

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/842,385
(B) FILING DATE: 23-APR-1997

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Becker, Cheryl L.
(B) REGISTRATION NUMBER: 35,441
(C) REFERENCE/DOCKET NUMBER: 6084.US.P1

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 847/935-1729
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(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 232 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCGCATCCG AGCCATGGCC CAGCAGGTGT TTATGCTGGA CACCCAGTGC TCACCAAAGA	60
CACCAAACAA CTTTGACCAC GCTCAGTCCT GCCAGCTCAT TATTGAGCTG CCTCCTGATG	120
AAAAACCAAA TGGACACACC AAGAAAAGCG TGTCTTCAG GGAAATTGTG GTGAGCCTGC	180
TGTCTCATCA GGTGTTACTC CAGAACTTAT ATGACATCTT GTTAGAAGAG TT	232

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 289 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTTTCAAGGGA AATTGTGGTG AGCCTGCTGT CTCATCAGGT GTTACTCCAG AACTTATATG	60
ACATCTTGTG AGAAGAGTTT GTCAAAGGCC CCTCTCCTGG AGAGGAAAAG ACGATACAAG	120
TGCCAGAACG CAAGCTGGCT GGCTTCCTCA GATACATCTC TATGCAGAAC TTGGCAGTCA	180
TATTCGACCT GCTGCTGGAC TCTTATAGGA CTGCCAGGGGA GTTTGACACC AGCCCCGGC	240
TGAAGTGCCT GCTGAAGAAA GTGTCTGGCA TCGGGGGCGC CGCCAACCT	289

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 264 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGCAGTCATA TTCGACCTGC TGCTGGACTC TTATAGGACT GCCAGGGAGT TTGACACCAG	60
CCCCGGGCTG AAGTGCCTGC TGAAGAAAGT GTCTGGCATC GGGGGCGCCG CCAACCTCTA	120
CCGCCAGTCT GCGATGAGTT TAACATTAT TTCCACGCC CGAGCAAGTG AAGAAGGTCC	180
AATCAAGAAA ACATCACGGC CGAGCAAGTG AAGAAGGTCC TTTTGAGGA CGACGAGAGA	240
AGCACGGATT CTTCCCAGCA GTGT	264

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 260 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CATATTGCAC CTGCTGCTGG ACTCTTATAG GACTGCCAGG GAGTTTGACA CCAGCCCCGG	60
GCTGAAGTGC CTGCTGAAGA AAGTGTCTGG CATCGGGGGC GCCGCCAAC TCTACCGCCA	120
GTCTGCGATG AGCTTTAAC A TTTATTTCCA CGCCCTGGTG TGTGCTGTT TCACCAATCA	180
AGAAACCATC ACGGGCGAGC AAGTGAAGAA GGTCCTTTT GAGGACGACG AGAGAAGCAC	240
GGATTCTTCC CAGCACTGTT	260

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCACTGGGTC	CCAGGGGCCA	GGACTCCCCG	CTGCTTCAGC	GTCCCCAGCA	CTTGATGGAC	60
CAAGGGCAA	TGCGGCATTC	CTTCAGCGCA	GGCCCCGAGC	TGCTGCGACA	GGACAAGAGG	120
CCCCGCTCAG	GCTCCACCGG	GAGCTCCCTC	AGTGTCTCGG	TGAGAGACGC	AGAACGCACAG	180
ATCAGGCATG	GACCAACAT					199

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CATTCCCTCA	GCGCAGGGCCC	CGAGCTGCTG	CGACAGGACA	AGAGGGCCCCG	CTCAGGCTCC	60
ACCGGGAGCT	CCCTCAGTGT	CTCGGTGAGA	GACGCAGAAG	CACAGATCCA	GGCATGGACC	120
AACATGGTGC	TAACAGTTCT	CAATCAGATT	CAGATTCTCC	CAGACCAGAC	CTTCACGGCC	180
CTCCAGCCCG	CAGTGTTCCTC	GTGCATCAGT	CAGCTGACCT	GTCACGTGAC	CGACATCAGA	240
GTTCGCAGG	CTGCGAGGGA	GTGGCTGGGC	AGGGTGGGCC	GTGTCTATGA	CATCATTGTG	300
TAGCCGACTC	CTGTTCTACT	CTCCCCACCAA	ATAACAGTAG	TGAGGGTTAG	AGTCCTGCCA	360
ATACAGCTGT	TGCATTTTCC	CCACCACTAG	CCCCACTTAA	ACTACTACTA	CTGTCTCAGA	420
GAACAGTGT	TCCTAATGTA	AAAAGCCTTT	CCAACCACTG	ATCAGCATT		470

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CACGGCCCTC	CAGCCCGCAG	TGTTCCCGTG	CATCAGTCAG	CTGACCTGTC	ACGTGACCGA	60
CATCAGAGTT	CGCCAGGCTG	TGAGGGAGTG	GCTGGCAGG	GTGGGCCGTG	TCTATGACAT	120
CATTGTGTAG	CCGACTCCTG	TTCTACTCTC	CCACCAAATA	ACAGTAGTGA	GGGTTAGAGT	180
CCTGCCAATA	CAGCTGTTGC	ATTTTCCCCA	CCACTAGCCC	CACTTAAACT	AC	232

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TAAGGTTTGT	ATCTAGATGA	CACAAACGAT	ATTCTGATTT	TGCACATTAT	TATAGAAGAA	60
TCTATAATCC	TTGATATGTT	TCTAACTCTT	GAAGTATATT	TCCCAGTGCT	TTTGCTTACA	120

GTGTTGTCCC CAAATGGTC ATTTCAGG ATTACTCATT TGAAAACACT ATATTGATCC	180
ATTTGATCCA TCATTTAAAA AATAAATACA ATTCCTAAGG CAATATCTGC TGGTAAGTCA	240
AGCT	244

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1771 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGCA GTCTACATA TTGACCTGC TGCTGGACTC TTATAGGACT GCCAGGGAGT TTGACACCAG	60
CCCCGGGCTG AAGTGCCTGC TGAAGAAAGT GTCTGGCATC GGGGGCGCCG CCAACCTCTA	120
CCGCCAGTCT GCGATGAGCT TTAACATTTA TTTCCACGCC CTGGTGTGTG CTGTTCTCAC	180
CAATCAAGAA ACCATCACCG CCGAGCAAGT GAAGAAGGTC CTTTTGAGG ACGACGAGAG	240
AAGCACGGAT TCTTCCCAGC AGTGTTCATC TGAGGATGAA GACATTTG AGGAAACCGC	300
CCAGGTCAAG CCCCGAGAG GCAAGGAGAA GAGACAGTGG CGGGCACCGA TGCCCCTTGCT	360
CAGCGTCCAG CCTGTCAAGCA ACGCAGATTG GGTGTGGCTG GTCAAGAGGC TGCAAGAGCT	420
GTGCATGGAA CTGTGCAACA ACTACATCCA GATGCACTTG GACCTGGAGA ACTGTATGGA	480
GGAGCCTCCC ATCTTCAAGG GCGACCCGTT CTTCATCCTG CCCTCCTTCC AGTCCGAGTC	540
ATCCACCCCA TCCACCGGGG GCTTCTCTGG GAAAGAAACC CTTCCGAGG ATGACAGAAC	600
CCAGTCCCGG GAGCACATGG GCGAGTCCCT GAGCCTGAAG GCGGTGGTG GGGACCTGCT	660
GCTGCCCGG AGCCCCAAAG TGGAGAAGAA GGATCCCAGC CGGAAGAAGG AGTGGTGGGA	720
GAATGCGGGG AACAAAATCT ACACATGGC AGCCGACAAG ACCATTTCAA AGTTGATGAC	780
CGAATACAAA AAGAGGAAAC AGCAGCACAA CCTGTCCCG GTTCCCAAAG AGGTCAAAGT	840
GGAGAAGAAA GGAGAGCCAC TGGGTCCCGAG GGGCCAGGAC TCCCCCTGCC TTCAGCGTCC	900
CCAGCACTTG ATGGACCAAG GGCACATGCG GCATTCCTTC AGCGCAGGCC CGAGCTGCT	960
GCGACAGGAC AAGAGGCCCG GCTCAGGCTC CACCGGGAGC TCCCTCAGTG TCTCGGTGAG	1020
AGACGCAGAA GCACAGATCC AGGCATGGAC CAACATGGTG CTAACAGTTC TCAATCAGAT	1080
TCAGATTCTC CCAGACCAGA CCTTCACCGC CCTCCAGCCC GCAGTGTTC CGTGCATCAG	1140
TCAGCTGACC TGTACGTGA CCGACATCAG AGTCGCCAG GCTGTGAGGG AGTGGCTGGG	1200
CAGGGTGGGC CGTGTCTATG ACATCATTGT GTAGCCGACT CCTGTTCTAC TCTCCCACCA	1260
AATAACAGTA GTGAGGGTTA GAGTCCTGCC ATACAGCTG TTGCATTTTC CCCACCACTA	1320
GCCCCACTTA AACTACTACT ACTGTCTCAG AGAACAGTGT TTCCCTAATGT AAAAAGCCTT	1380
TCCAACCACT GATCAGCAGA GGGGCCATT TAAGGTTGT ATCTAGATGA CACAAACGAT	1440
ATTCTGATTT TGACACATTAT TATAGAAGAA TCTATAATCC TTGATATGTT TCTAACTCTT	1500
GAAGTATATT TCCCAGTGT TTTGCTTACA GTGTTGTCCC CAAATGGTC ATTTTCAAGG	1560
ATTACTCATT TGAAAACACT ATATTGATCC ATTGATCCA TCATTTAAAA AATAAATACA	1620
ATTCTAAGG CAATATCTGC TGGTAAGTCA AGCTGATAAA CACTCAGACA TCTAGTACCA	1680
GGGATTATTA ATTGGAGGAA GATTTATGGT TATGGGTCTG GCTGGGAAGA AGACAACATAT	1740
AAATACATAT TCTTGGGTGT CATAATCAAG A	1771

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2096 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGCGCATCCG AGCCATGGCC CAGCAGGTGT TTATGCTGGA CACCCAGTGC TCACCAAAGA	60
CACCAAACAA CTTTGACCAC GCTCAGTCCT GCCAGCTCAT TATTGAGCTG CCTCCTGATG	120
AAAAACCAA TGGACACACC AAGAAAAGCG TGTCTTTCAG GGAAATTGTG GTGAGCCTGC	180
TGTCTCATCA GGTGTTACTC CAGAACTTAT ATGACATCTT GTTAGAAGAG TTTGTCAAAG	240
GCCCCCTCTCC TGGAGAGGAA AAGACGATAC AAGTGCAGA AGCCAAGCTG GCTGGCTTCC	300
TCAGATACAT CTCTATGCAG AACCTGGCAG TCATATTGCA CCTGCTGCTG GACTCTTATA	360
GGACTGCCAG GGAGTTGAC ACCAGCCCCG GGCTGAAGTG CCTGCTGAAG AAAGTGTCTG	420
GCATCGGGGG CGCCGCCAAC CTCTACCGCC AGTCTGCGAT GAGCTTAAAC ATTTATTTCC	480
ACGCCCTGGT GTGTGCTGTT CTCACCAATC AAGAAACCAC CACGGCGAG CAAGTGAAGA	540

AGGTCTTTT	TGAGGACGAC	GAGAGAAGCA	CGGATTCTTC	CCAGCAGTGT	TCATCTGAGG	600
ATGAAGACAT	CTTGAGGAA	ACCGCCAGG	TCAGCCCCC	GAGAGGCAAG	GAGAAGAGAC	660
AGTGGCGGGC	ACGGATGCC	TTGCTCAGCG	TCCAGCCTGT	CAGCAACGCA	GATTGGGTGT	720
GGCTGGTCAA	GAGGCTGCAC	AAGCTGTCA	TGGAACGTGT	CAACAACATAC	ATCCAGATGC	780
ACTTGGACCT	GGAGAACTGT	ATGGAGGAGC	CTCCCATCTT	CAAGGGCGAC	CCGTTCTTCA	840
TCCTGCCCTC	CTTCCAGTCC	GAGTCATCCA	CCCCATCCAC	CGGGGGCTTC	TCTGGGAAAG	900
AAACCCCTTC	CGAGGATGAC	AGAAGCCAGT	CCCAGGAGCA	CATGGGCGAG	TCCCTGAGCC	960
TGAAGGCCGG	TGGTGGGGAC	CTGCTGCTGC	CCCCCAGCCC	CAAAGTGGAG	AAGAAGGATC	1020
CCAGCCGGAA	GAAGGAGTGG	TGGGAGAATG	CGGGGAACAA	AATCTACACC	ATGGCAGCCG	1080
ACAAGACCAT	TTCAAAGTTG	ATGACCGAAT	ACAAAAAAGAG	GAAACAGCAG	CACAACCTGT	1140
CCGCGTTCCC	CAAAGAGGTC	AAAGTGGAGA	AGAAAGGAGA	GCCACTGGGT	CCCAGGGGCC	1200
AGGACTCCCC	GCTGCTTCAG	CGTCCCCAGC	ACTTGATGGA	CCAAGGGCAA	ATGCGGCATT	1260
CCTTCAGCGC	AGGGCCCCAG	CTGCTGCCAG	AGGACAAGAG	CCCCCGCTCA	GGCTCACCG	1320
GGAGCTCCCT	CAGTGTCTCG	GTGAGAGACG	CAGAACACA	GATCCAGGGC	TGGACCAACA	1380
TGGTGCTAAC	AGTTCTCAAT	CAGATTCA	TTCTCCCAGA	CCAGACCTTC	ACGGCCCTCC	1440
AGCCCGCAGT	GTTCCCGTGC	ATCAGTCAGC	TGACCTGTCA	CGTGACCGAC	ATCAGAGTTC	1500
GCCAGGCTGT	GAGGGAGTGG	CTGGGCAGGG	TGGGCCGTGT	CTATGACATC	ATTGTGTAGC	1560
CGACTCCTGT	TCTACTCTCC	CACCAAATAA	CAGTAGTGAG	GGTTAGAGTC	CTGCCAATAC	1620
AGCTGTTGCA	TTTCCCCAC	CACTAGCCCC	ACTTAAACTA	CTACTACTGT	CTCAGAGAAC	1680
AGTGTTCCT	AATGTAAAAA	GCCTTTCCAA	CCACTGATCA	GCATTRGGGC	CATACTAAGG	1740
TTTGATCTA	GATGACACAA	ACGATATTCT	GATTTGCAC	ATTATTATAG	AAGAATCTAT	1800
AATCTTGAT	ATGTTCTAA	CTCTTGAAGT	ATATITCCC	GTGCTTTTG	TTACAGTGT	1860
GTCCCCAAAT	GGGTCTATT	CAAGGATTAC	TCATTGAAA	ACACTATT	GATCCATTG	1920
ATCCATCATT	TAAAAAAATA	ATACAATTCC	TAAGGCAATA	TCTGCTGGTA	AGTCAAGCTG	1980
ATAAACACTC	AGACATCTAG	TACCAAGGGAT	TATTAATTGG	AGGAAGATT	ATGGTTATGG	2040
GTCTGGCTGG	GAAGAAGACA	ACTATAATA	CATATTCTTG	GGTGTCAAA	TCAAGA	2096

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGCTCGGAAT TCCGAGCTTG GATCCTCTAG AGCGGCCGCC GACTAGTGAG CTCGTCGACC
CGGGAATT

60
68

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AATTAATTCC CGGGTCGACG AGCTCACTAG TCGGGGGCCG CTCTAGAGGA TCCAAGCTCG
GAATTCCG

60
68

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGCGGATAAC AATTCACAC AGGA

24

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGTAAAACGA CGGCCAGT

18

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CACCAATCAA GAAACCATC

19

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCTCCAGCCC GCAGTGTTC

20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CTAGATGACA CAAACGATA

19

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AGGATGACAG AAGCCAGT

18

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AGCAAAAGCA CTGGGAAA

18

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CCCAGCCACT CCCTCACAGC

20

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GACTGGCGGT AGAGGTTGG

19

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ACAGTTCCAT GCACAGCTTG

20

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GAGGTCAAAG TGGAGAACAG AGGAG

25

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCTGTATTGG CAGGACTCTA ACCC

24.

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GCCGCCATGG ACCTGCTGCT GGACTCTTAT AG

32

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GCGGCCGCCCA ACAATGATGT CATAGACACG

30

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 518 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Arg	Ile	Arg	Ala	Met	Ala	Gln	Gln	Val	Phe	Met	Leu	Asp	Thr	Gln	Cys
1						5			10					15	
Ser	Pro	Lys	Thr	Pro	Asn	Asn	Phe	Asp	His	Ala	Gln	Ser	Cys	Gln	Leu
			20				25					30			
Ile	Ile	Glu	Leu	Pro	Pro	Asp	Glu	Lys	Pro	Asn	Gly	His	Thr	Lys	Lys
		35				40		45							
Ser	Val	Ser	Phe	Arg	Glu	Ile	Val	Val	Ser	Leu	Leu	Ser	His	Gln	Val
	50		55		60										
Leu	Leu	Gln	Asn	Leu	Tyr	Asp	Ile	Leu	Leu	Glu	Glu	Phe	Val	Lys	Gly
	65				70		75			80					
Pro	Ser	Pro	Gly	Glu	Glu	Lys	Thr	Ile	Gln	Val	Pro	Glu	Ala	Lys	Leu
	85					90			95						
Ala	Gly	Phe	Leu	Arg	Tyr	Ile	Ser	Met	Gln	Asn	Leu	Ala	Val	Ile	Phe
			100				105				110				

Asp Leu Leu Leu Asp Ser Tyr Arg Thr Ala Arg Glu Phe Asp Thr Ser
115 120 125
Pro Gly Leu Lys Cys Leu Leu Lys Lys Val Ser Gly Ile Gly Gly Ala
130 135 140
Ala Asn Leu Tyr Arg Gln Ser Ala Met Ser Phe Asn Ile Tyr Phe His
145 150 155 160
Ala Leu Val Cys Ala Val Leu Thr Asn Gln Glu Thr Ile Thr Ala Glu
165 170 175
Gln Val Lys Lys Val Leu Phe Glu Asp Asp Glu Arg Ser Thr Asp Ser
180 185 190
Ser Gln Gln Cys Ser Ser Glu Asp Glu Asp Ile Phe Glu Glu Thr Ala
195 200 205
Gln Val Ser Pro Pro Arg Gly Lys Glu Lys Arg Gln Trp Arg Ala Arg
210 215 220
Met Pro Leu Leu Ser Val Gln Pro Val Ser Asn Ala Asp Trp Val Trp
225 230 235 240
Leu Val Lys Arg Leu His Lys Leu Cys Met Glu Leu Cys Asn Asn Tyr
245 250 255
Ile Gln Met His Leu Asp Leu Glu Asn Cys Met Glu Glu Pro Pro Ile
260 265 270
Phe Lys Gly Asp Pro Phe Phe Ile Leu Pro Ser Phe Gln Ser Glu Ser
275 280 285
Ser Thr Pro Ser Thr Gly Gly Phe Ser Gly Lys Glu Thr Pro Ser Glu
290 295 300
Asp Asp Arg Ser Gln Ser Arg Glu His Met Gly Glu Ser Leu Ser Leu
305 310 315 320
Lys Ala Gly Gly Asp Leu Leu Leu Pro Pro Ser Pro Lys Val Glu
325 330 335
Lys Lys Asp Pro Ser Arg Lys Lys Glu Trp Trp Glu Asn Ala Gly Asn
340 345 350
Lys Ile Tyr Thr Met Ala Ala Asp Lys Thr Ile Ser Lys Leu Met Thr
355 360 365
Glu Tyr Lys Lys Arg Lys Gln Gln His Asn Leu Ser Ala Phe Pro Lys
370 375 380
Glu Val Lys Val Glu Lys Lys Gly Glu Pro Leu Gly Pro Arg Gly Gln
385 390 395 400
Asp Ser Pro Leu Leu Gln Arg Pro Gln His Leu Met Asp Gln Gly Gln
405 410 415
Met Arg His Ser Phe Ser Ala Gly Pro Glu Leu Leu Arg Gln Asp Lys
420 425 430
Arg Pro Arg Ser Gly Ser Thr Gly Ser Ser Leu Ser Val Ser Val Arg
435 440 445
Asp Ala Glu Ala Gln Ile Gln Ala Trp Thr Asn Met Val Leu Thr Val
450 455 460
Leu Asn Gln Ile Gln Ile Leu Pro Asp Gln Thr Phe Thr Ala Leu Gln
465 470 475 480
Pro Ala Val Phe Pro Cys Ile Ser Gln Leu Thr Cys His Val Thr Asp
485 490 495
Ile Arg Val Arg Gln Ala Val Arg Glu Trp Leu Gly Arg Val Gly Arg
500 505 510
Val Tyr Asp Ile Ile Val
515

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Glu Asp Asp Glu Arg Ser Thr Asp Ser Ser Gln Gln Cys Ser Ser Glu
1 5 10 15
Asp Glu Asp Ile Phe Glu Glu Thr Ala Gln Val Ser Pro Pro Arg Gly
20 25 30
Lys Glu Lys Arg Gln Trp Arg Ala Arg
35 40

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Ser Phe Gln Ser Glu Ser Ser Thr Pro Ser Thr Gly Gly Phe Ser Gly
1 5 10 15
Lys Glu Thr Pro Ser Glu Asp Asp Arg Ser Gln Ser Arg Glu His Met
20 25 30
Gly Glu Ser
35

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Ser Pro Lys Val Glu Lys Lys Asp Pro Ser Arg Lys Lys Glu Trp Trp
1 5 10 15
Glu Asn Ala Gly Asn Lys Ile Tyr Thr Met Ala Ala Asp Lys Thr Ile
20 25 30
Ser Lys Leu Met Thr Glu Tyr Lys
35 40

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Glu Pro Leu Gly Pro Arg Gly Gln Asp Ser Pro Leu Leu Gln Arg Pro
1 5 10 15
Gln His Leu Met Asp Gln Gly Gln Met Arg His Ser Phe Ser Ala Gly
20 25 30
Pro Glu Leu Leu Arg Gln Asp Lys Arg Pro Arg Ser Gly Ser Thr Gly
35 40 45
Ser

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Met His Thr Glu His
1 5 10 15
His His His His His
20